

1

Figure 1A. Nucleic acid encoding human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:1)

```
1 TACTGGAAGGTGGCGTGCCCTCCTCTGGCTGGTACCATGCAGCTCCCACT
51 GGCCCTGTGTCTCGTCTGCCTGCTGGTACACACAGCCTTCCGTGTAGTGG
101 AGGGCCAGGGGTGGCAGGCGTTCAAGAATGATGCCACGGAAATCATCCCC
151 GAGCTCGGAGAGTACCCCGAGCCTCCACCGAGCTGGAGAAACAACAAGAC
201 CATGAACCGGGCGGAGAACGGAGGGCGGCCTCCCCACCACCCCTTTGAGA
251 CCAAAGACGTGTCCGAGTACAGCTGCCGCGAGCTGCACTTCACCCGCTAC
301 GTGACCGATGGGCCGTGCCGAGCGCCAAGCCGGTCACCGAGCTGGTGTG
351 CTCGGGCCAGTGCAGCCCGGCGCGCCTGCTGCCAACGCCATCGGCCGCG
401 GCAAGTGGTGGCGACCTAGTGGGCCCGACTTCGCTGCATCCCCGACCGC
451 TACCGCGCGCAGCGCGTGCAGCTGCTGTGTCCCGGTGGTGAGGCGCCGCG
501 CGCGCGCAAGGTGCGCCTGGTGGCCTCGTGCAAGTGCAAGCGCCTCACCC
551 GCTTCCACAACCAGTCGGAGCTCAAGGACTTCGGGACCGAGGCCGCTCGG
601 CCGCAGAAGGGCCGGAAGCCGCGGCCCGCGCCCGGAGCGCCAAAGCCAA
651 CCAGGCCGAGCTGGAGAAGCGCTACTAGAGCCCGCCCGCGCCCTCCCCA
701 CCGGCGGGCGCCCCGCCCTGAACCCGCGCCCCACATTTCTGTCTCTGC
751 GCGTGGTTT
```

B. Human Cloaked-2 polypeptide most likely mature form (SEQ ID NO:2)

```
1 QGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAENGGRPPHHPFETK
51 DVSEYSCRELHFTRYVTDGPCRSAPVTELVCSGQCGPARLLPNAIGRGK
101 WWRPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRF
151 HNQSELKDFGTEAARPQKGRKPRPRARSAKANQAELENAY
```

C. Human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:5)

```
1 MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATEIIPELGEYPEPPPEL
51 ENNKTMNRAENGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAPV
101 TELVCSGQCGPARLLPNAIGRGKWWRPSPGDFRCIPDRYRAQRVQLLCPG
151 GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR
201 SAKANQAELENAY
```

2

Figure 2A. Nucleic acid encoding mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:3)

```
1 ATGCAGCCCTCACTAGCCCCGTGCCTCATCTGCCTACTTGTGCACGCTGC
51 CTTCTGTGCTGTGGAGGGCCAGGGGTGGCAAGCCTTCAGGAATGATGCCA
101 CAGAGGTATCCCAGGGCTTGGAGAGTACCCCGAGCCTCCTCTGAGAAC
151 AACCAGACCATGAACCGGGCGGAGAATGGAGGCAGACCTCCCCACCATCC
201 CTATGACGCCAAGATGTGTCCGAGTACAGCTGCCGCGAGCTGCACTACA
251 CCCGCTTCTGTACAGACGGCCCATGCCGCGAGCGCAAGCCGGTCACCGAG
301 TTGGTGTGCTCCGGCCAGTGCGGCCCCGCGCGGCTGCTGCCCAACGCCAT
351 CGGGCGCGTGAAGTGGTGGCGCCCGAACGGACCGGATTTCGCTGCATCC
401 CGGATCGCTACCGCGCGCAGCGGGTGCAGCTGCTGTGCCCGGGGGCGCG
451 GCGCCGCGCTCGCGCAAGGTGCGTCTGGTGGCCTCGTGCAAGTGCAAGCG
501 CCTCACCCTTCCACAACAGTCGGAGCTCAAGGACTTCGGGCGCGAGA
551 CCGCGCGCCCGCAGAAGGGTCGCAAGCCGCGCCCGGCGCCCGGGGAGCC
601 AAAGCCAACCAGGCGGAGCTGGAGAACGCCTACTAG
```

B. Mouse Cloaked-2 polypeptide most likely mature form (SEQ ID NO:4)

```
1 QGWQAFRNDATEVIPGLGEYPEPPPENQTMNRAENGGRPPHHPYDAKDV
51 SEYSCRELHYTRFLTDGPCRSAPVTELVCSGQCGPARLLPNAIGRVKWW
101 RPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHN
151 QSELKDFGPETARPQKGRKPRPGARGAKANQAELENAY
```

C. Mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:6)

```
1 MQPSLAPCLICLLVHAAFCAVEGQGWQAFRNDATEVIPGLGEYPEPPPEN
51 NQTMNRAENGGRPPHHPYDAKDVSEYSCRELHYTRFLTDGPCRSAPVTE
101 LVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPGGA
151 APRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGARGA
201 KANQAELENAY
```

### Figure 3

GAP of: Human Cloaked-2 check: 5775 from: 1 to: 213  
 to: Mouse Cloaked-2 check: 9489 from: 1 to: 211

Symbol comparison table:  
 /GCGDISK/gcg10/gcgcore/data/rundata/blosum62.cmp  
 CompCheck: 6430

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	1028	Length:	213
Ratio:	4.872	Gaps:	1
Percent Similarity:	91.469	Percent Identity:	88.152

Match display thresholds for the alignment(s):  
 | = IDENTITY  
 : = 2  
 . = 1

#### Human Cloaked-2 (SEQ ID NO: 5) x Mouse Cloaked-2 (SEQ ID NO: 6)

```

1 MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATETIIPELGEYPEPPPEL 50
  || || |:|||| | ||||| |:|:| |||||
1 MQPSLAPCLICLLVHA AFCAVEGQGWQAFRNDATEVIPGLGEYPEPPP.. 48

51 ENNKTMNRAENGGRPPHHPFETKDVSEYSCRELHFPTRYVTDGPCRSAKPV 100
  |||.|||||:|: ||||| |:|. |||||
49 ENNQTMNRAENGGRPPHHPYDAKDVSEYSCRELHYTRFLT DGPCRSAKPV 98

101 TELVCSGQC GPARLLPNAIGRGKWWRPSPGDFRCIPDRYRAQRVQLLCPG 150
  ||||| |||||. ||||| |||||
99 TELVCSGQC GPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPG 148

151 GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR 200
  | |||. ||||| ||||| ||||| | |||||
149 GAAPRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGAR 198

201 SAKANQAELENAY 213
  |||||
199 GAKANQAELENAY 211
    
```

```

1 .....FKNDATEILYSHVVKP.VPAHPSSNSTLNQARNGGRHFSNTGLDR 44
  ||||| : | :|:| | | | :
1 QGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAENGGRP.PHHPFET 49
  : |||| | :|:| | | | | . ||| | | |
45 NTRVQVGCRELRSTKYISDGOCTSI SPLKELVCAGECLPLPVLPNWIGGG 94
  : |||| | :|:| | | | | . ||| | | |
50 KDVSEYSCRELHFTRYVTDGPCRSAPVTELVCSGQCGPARLLPNAIGRG 99
  : |||| | :|:| | | | | . ||| | | |
95 YGTTYWSRRSSQEWRCVNDKTRTORIQLQCDG.STRTYKITVVTACKCK 143
  | :| | | :. || : | : | | :| | | . | | : . | | |
100 ...KWW.RPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCK 145
  : |||| | :|:| | | | | . ||| | | |
144 RYTRQHNESSHNFE SMSPAKPVQHHRERKRASKSSKHSMS..... 183
  | ||| | :| | : | | :| . | .
146 RLTRFHNQSELKDFGTEAARPQKGRKPRPRA.RSAKANQAELENAY 190

```